

METHOD FOR DETECTION OF MULTIPLE NUCLEIC ACID SEQUENCE VARIATIONS

ABSTRACT OF THE DISCLOSURE

A method for detecting the presence or absence of a genetic variation at a polymorphic site in a nucleic acid analyte in a sample is provided. The method comprises a series of steps used to form captured wild type complexes and captured variant complexes that are detected and counted. The method is carried out using first and second differential hybridization probes, first and second capture probes, and first and second solid substrates, each having a detectable signal. The invention also provides for kits for carrying out the assay.